oxo-dG is used as a nucleotide substrate of the polymerase in conjunction with PCR to randomly or stochastically interchange T and G and consequently complementary interchange A and C. This is therefore a PCR mediated random transversion mutagenesis, converting T to G and A to C, but not the converse (e.g., neither G to T nor C to A).

IN THE CLAIMS:

Please cancel claims 40-114 without prejudice or disclaimer with respect to any future prosecution on the subject matter set forth therein.

Please amend claims 1-7, 14, 17, 18, 20, 22-24, 34, 37, and 38, as indicated in Appendix B. The amended claims will then read as follows:

1. **(Amended)** A method of employing oligonucleotide probes to obtain information on a target nucleic acid analyte containing a target sequence segment, the method comprising:

contacting the analyte, under hybridizing conditions, with at least two oligonucleotide probes, each oligonucleotide probe comprising a sequence segment complementary to the target sequence or complementary to the target sequence except at a position of interest,

wherein each of the at least two oligonucleotide probes has one nucleotide capable of base pairing with a set of two or more nucleotides, said set of two or more nucleotides including one nucleotide common to all sets and lacking one nucleotide present in the target sequence segment; and

wherein hybridization of each oligonucleotide probe to the target sequence segment under the hybridizing conditions occurs only if no mismatch exists at the position of interest, such that depending upon the identity of the nucleotide at the position of interest, all, some or none of the at least two oligonucleotide probes hybridize to the target sequence segment.

2. **(Amended)** The method of claim 1 wherein the target sequence segment of the analyte has four nucleotides and at least two oligonucleotide probes are used, each oligonucleotide probe comprising, at a position corresponding to the position of interest, a nucleotide base pairing with two of the four nucleotides present in the target sequence segment.

3. **(Amended)** The method of claim 1 wherein the target sequence segment of the analyte has at least five nucleotides and at least three oligonucleotide probes are used, each oligonucleotide probe comprising, at a position corresponding to the position of interest, a nucleotide base pairing with at least three of the at least five nucleotides present in the target sequence segment.

4. **(Amended)** The method of claim 3 wherein the target sequence segment of the analyte has five nucleotides and three oligonucleotide probes are used, each oligonucleotide probe comprising at a position corresponding to a variable position of the target sequence segment, a nucleotide base pairing with a set of two or three nucleotides, wherein the sets having nucleic acid sequences in common each lack at least one nucleotide not common to the sets.

5. **(Amended)** The method of claim 1 further comprising a null hybridizing sequence comprising a nucleic acid sequence complementary to the target sequence segment,

wherein the null hybridizing sequence is base paired with a set of two or more nucleotides at a variable position of the target sequence segment; and

wherein a nucleotide represented in neither a first or second set of the two or more nucleotides at the variable position is used to probe the target sequence segment.

6. **(Amended)** The method of claim 1 used for sequencing the target nucleic acid analyte.

7. **(Amended)** The method of claim 6, further comprising an array of oligonucleotide probes, wherein the sequence of the target nucleic acid analyte is determined by analysis of hybridization data obtained from the array of oligonucleotide probes.

14. **(Amended)** The method of claim 9 wherein detection of a target sequence segment hybridizing to an oligonucleotide probe is by detection of a target signal.

17. **(Amended)** The method of claim 6 wherein the sequencing method is by detection of labels that attach by hybridization to the target sequence segment.

18. **(Amended)** The method of claim 1 wherein hybridized target nucleic acids are amplified by a polymerase enzyme that requires a hybridized complex for amplifying a nucleic acid sequence.

20. **(Amended)** The method of claim 18 wherein hybridized nucleic acids are amplified by an RNA replicase enzyme.

22. **(Amended)** The method of claim 1 used for allelic analysis.

23. **(Amended)** The method of claim 1 wherein the target nucleic acid analyte is derived from genomic DNA.

24. **(Amended)** The method of claim 1 wherein the target nucleic acid analyte is derived from a cDNA.

34. **(Amended)** The method of claim 33 wherein the second label moiety comprises a luminescent moiety.

37. **(Amended)** The method of claim 36 wherein the hybridization is enhanced by increasing hybridization stringency.

38. **(Amended)** The method of claim 39 wherein the electric potential at the substrate surface is electronically controlled to enhance hybridization.